

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/579,622
Source: IFWP
Date Processed by STIC: 5/26/06

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/579,622

DATE: 05/26/2006

TIME: 08:14:03

Input Set : A:\Sequence Listing.txt
 Output Set: N:\CRF4\05262006\J579622.raw

5 <110> APPLICANT: Crusade Laboratories Limited
 7 Sloane-Kettering Institute for Cancer Research
 9 Brown, Susanne M
 11 Dunn, Paul
 13 Singh, Bhuvanesh
 15 Ganly, Ian
 19 <120> TITLE OF INVENTION: Mutant Viruses
 23 <130> FILE REFERENCE: 6947-75757-01
 C--> 27 <140> CURRENT APPLICATION NUMBER: US/10/579,622
 C--> 27 <141> CURRENT FILING DATE: 2006-05-16
 27 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/004908
 29 <151> PRIOR FILING DATE: 2004-11-17
 33 <150> PRIOR APPLICATION NUMBER: GB 0326798.6
 35 <151> PRIOR FILING DATE: 2003-11-17
 39 <150> PRIOR APPLICATION NUMBER: US 60/541,308
 41 <151> PRIOR FILING DATE: 2004-02-03
 45 <160> NUMBER OF SEQ ID NOS: 6
 49 <170> SOFTWARE: PatentIn version 3.1
 53 <210> SEQ ID NO: 1
 55 <211> LENGTH: 918
 57 <212> TYPE: DNA
 59 <213> ORGANISM: Homo sapiens
 63 <220> FEATURE:
 65 <221> NAME/KEY: CDS
 67 <222> LOCATION: (58)..(837)
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 74 atg aac aag ttg aaa tca tcg cag aag gat aaa gtt cgt cag ttt atg 105
 75 Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
 76 1 5 10 15
 78 atc ttc aca caa tct agt gaa aaa aca gca gta agt tgt ctt tct caa 153
 79 Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
 80 20 25 30
 82 aat gac tgg aag tta gat gtt gca aca gat aat ttt ttc caa aat cct 201
 83 Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
 84 35 40 45
 86 gaa ctt tat ata cga gag agt gta aaa gga tca ttg gac agg aag aag 249
 87 Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
 88 50 55 60
 90 tta gaa cag ctg tac aat aga tac aaa gac cct caa gat gag aat aaa 297
 91 Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys
 92 65 70 75 80
 94 att gga ata gat ggc ata cag cag ttc tgt gat gac ctg gca ctc gat 345

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99	Pro	Ala	Ser	Ile	Ser	Val	Leu	Ile	Ile	Ala	Trp	Lys	Phe	Arg	Ala	Ala	
100							100			105					110		
102	aca	cag	tgc	gag	ttc	tcc	aaa	cag	gag	ttc	atg	gat	ggc	atg	aca	gaa	441
103	Thr	Gln	Cys	Glu	Phe	Ser	Lys	Gln	Glu	Phe	Met	Asp	Gly	Met	Thr	Glu	
104							115			120					125		
106	tta	gga	tgt	gac	agc	ata	gaa	aaa	cta	aag	gcc	cag	ata	ccc	aag	atg	489
107	Leu	Gly	Cys	Asp	Ser	Ile	Glu	Lys	Leu	Lys	Ala	Gln	Ile	Pro	Lys	Met	
108							130			135					140		
110	gaa	caa	gaa	ttg	aaa	gaa	cca	gga	cga	ttt	aag	gat	ttt	tac	cag	ttt	537
111	Glu	Gln	Glu	Leu	Lys	Glu	Pro	Gly	Arg	Phe	Lys	Asp	Phe	Tyr	Gln	Phe	
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114	act	ttt	aat	ttt	gca	aag	aat	cca	gga	caa	aaa	gga	tta	gat	cta	gaa	585
115	Thr	Phe	Asn	Phe	Ala	Lys	Asn	Pro	Gly	Gln	Lys	Gly	Leu	Asp	Leu	Glu	
116							165			170					175		
118	atg	gcc	att	gcc	tac	tgg	aac	tta	gtg	ttt	aat	gga	aga	ttt	aaa	ttc	633
119	Met	Ala	Ile	Ala	Tyr	Trp	Asn	Leu	Leu	Asn	Gly	Arg	Phe	Lys	Phe		
120							180			185					190		
122	tta	gac	tta	tgg	aat	aaa	ttt	ttg	ttg	gaa	cat	cat	aaa	cga	tca	ata	681
123	Leu	Asp	Leu	Trp	Asn	Lys	Phe	Leu	Leu	Glu	His	His	Lys	Arg	Ser	Ile	
124							195			200					205		
126	cca	aaa	gac	act	tgg	aat	ctt	ctt	tta	gac	ttc	agt	acg	atg	att	gca	729
127	Pro	Lys	Asp	Thr	Trp	Asn	Leu	Leu	Asp	Phe	Ser	Thr	Met	Ile	Ala		
128							210			215					220		
130	gat	gac	atg	tct	aat	tat	gat	gaa	gaa	gca	tgg	cct	gtt	ctt	att		777
131	Asp	Asp	Met	Ser	Asn	Tyr	Asp	Glu	Glu	Gly	Ala	Trp	Pro	Val	Leu	Ile	
132	225						230				235					240	
134	gat	gac	ttt	gtg	gaa	ttt	gca	cgc	cct	caa	att	gct	ggg	aca	aaa	agt	825
135	Asp	Asp	Phe	Val	Glu	Phe	Ala	Arg	Pro	Gln	Ile	Ala	Gly	Thr	Lys	Ser	
136							245			250					255		
138	aca	aca	gtg	tag	cactaaagga	accttctaga	atgtacatag	tctgtacaat									877
139	Thr	Thr	Val														
142	aaataacaaca	gaaaattgca	cagtcaattt	ctgctggctg	g												918
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161	Ile	Phe	Thr	Gln	Ser	Ser	Glu	Lys	Thr	Ala	Val	Ser	Cys	Leu	Ser	Gln	
162							20			25					30		
165	Asn	Asp	Trp	Lys	Leu	Asp	Val	Ala	Thr	Asp	Asn	Phe	Phe	Gln	Asn	Pro	
166							35			40					45		
169	Glu	Leu	Tyr	Ile	Arg	Glu	Ser	Val	Lys	Gly	Ser	Leu	Asp	Arg	Lys	Lys	
170							50			55					60		
173	Leu	Glu	Gln	Leu	Tyr	Asn	Arg	Tyr	Lys	Asp	Pro	Gln	Asp	Glu	Asn	Lys	

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Input Set : A:\Sequence Listing.txt
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181	Pro	Ala	Ser	Ile	Ser	Val	Leu	Ile	Ile	Ala	Trp	Lys	Phe	Arg	Ala	Ala												
182							100			105					110													
185	Thr	Gln	Cys	Glu	Phe	Ser	Lys	Gln	Glu	Phe	Met	Asp	Gly	Met	Thr	Glu												
186							115			120					125													
189	Leu	Gly	Cys	Asp	Ser	Ile	Glu	Lys	Leu	Lys	Ala	Gln	Ile	Pro	Lys	Met												
190							130			135					140													
193	Glu	Gln	Glu	Leu	Lys	Glu	Pro	Gly	Arg	Phe	Lys	Asp	Phe	Tyr	Gln	Phe												
194	145						145			150					155													
197	Thr	Phe	Asn	Phe	Ala	Lys	Asn	Pro	Gly	Gln	Lys	Gly	Leu	Asp	Leu	Glu												
198							195			200					170													
201	Met	Ala	Ile	Ala	Tyr	Trp	Asn	Leu	Val	Leu	Asn	Gly	Arg	Phe	Lys	Phe												
202							202			180					185													
205	Leu	Asp	Leu	Trp	Asn	Lys	Phe	Leu	Leu	Glu	His	His	Lys	Arg	Ser	Ile												
206							206			205					205													
209	Pro	Lys	Asp	Thr	Trp	Asn	Leu	Leu	Leu	Asp	Phe	Ser	Thr	Met	Ile	Ala												
210							210			215					220													
213	Asp	Asp	Met	Ser	Asn	Tyr	Asp	Glu	Glu	Gly	Ala	Trp	Pro	Val	Leu	Ile												
214	225						225			230					235													
217	Asp	Asp	Phe	Val	Glu	Phe	Ala	Arg	Pro	Gln	Ile	Ala	Gly	Thr	Lys	Ser												
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246							1			5					10													
248	cgt	cag	ttt	atg	atc	ttc	aca	caa	tct	agt	gaa	aaa	aca	gca	gta	agt		99										
249	Arg	Gln	Phe	Met	Ile	Phe	Thr	Gln	Ser	Ser	Glu	Lys	Thr	Ala	Val	Ser												
250							15			20					25													
252	tgt	ctt	tct	caa	aat	gac	tgg	aag	tta	gat	gtt	gca	aca	gat	aat	ttt		147										
253	Cys	Leu	Ser	Gln	Asn	Asp	Trp	Lys	Leu	Asp	Val	Ala	Thr	Asp	Asn	Phe												
254							30			35					40													
256	ttc	caa	aat	cct	gaa	ctt	tat	ata	cga	gag	agt	gta	aaa	gga	tca	ttg		195										
257	Phe	Gln	Asn	Pro	Glu	Leu	Tyr	Ile	Arg	Glu	Ser	Val	Lys	Gly	Ser	Leu												
258							45			50					55													60
260	gac	agg	aag	aag	tta	gaa	cag	ctg	tac	aat	aga	tac	aaa	gac	cct	caa			243									
261	Asp	Arg	Lys	Lys	Leu	Glu	Gln	Leu	Tyr	Asn	Arg	Tyr	Lys	Asp	Pro	Gln												
262							65			70					75													
264	gat	gag	aat	aaa	att	gga	ata	gat	ggc	ata	cag	cag	ttc	tgt	gat	gac			291									
265	Asp	Glu	Asn	Ile	Gly	Ile	Asp	Gly	Ile	Gln	Gln	Phe	Cys	Asp	Asp													

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268	ctg gca ctc gat cca gcc agc att agt gtg ttg att att	gct tgg aag		339
269	Leu Ala Leu Asp Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys			
270	95	100	105	
272	tcc aga gca gca aca cag tgc gag ttc tcc aaa cag gag ttc atg gat			387
273	Phe Arg Ala Ala Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp			
274	110	115	120	
276	ggc atg aca gaa tta gga tgt gac agc aca gaa aaa cta aag gcc cag			435
277	Gly Met Thr Glu Leu Gly Cys Asp Ser Thr Glu Lys Leu Lys Ala Gln			
278	125	130	135	140
280	ata ccc aag atg gaa caa gaa ttg aaa gaa cca gga cga ttt aag gat			483
281	Ile Pro Lys Met Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp			
282	145	150	155	
284	ttt tac cag ttt act ttt aat ttt gca aag aat cca gga caa aaa gga			531
285	Phe Tyr Gln Phe Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly			
286	160	165	170	
288	tta gat cta gaa atg gcc att gcc tac tgg aac tta gtg ctt aat gga			579
289	Leu Asp Leu Glu Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly			
290	175	180	185	
292	aga ttt aga ctc tta gac tta tgg aat aaa ttt ttg ttg gaa cat cat			627
293	Arg Phe Arg Leu Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His			
294	190	195	200	
296	aaa cga tca ata cca aaa gac act tgg aat ctt ctt tta gac ttc agt			675
297	Lys Arg Ser Ile Pro Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser			
298	205	210	215	220
300	acg atg att gca gat gac atg tct aat tat gat gaa gaa gga gca tgg			723
301	Thr Met Ile Ala Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp			
302	225	230	235	
304	cct gtt ctt att gat gac ttt gtg gaa ttt gca cgc cct caa att gct			771
305	Pro Val Leu Ile Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala			
306	240	245	250	
308	ggg aca aaa agt aca aca gtg tag cactaaagga accttctaga atgtacatag			825
309	Gly Thr Lys Ser Thr Thr Val			
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321	<213> ORGANISM: Homo sapiens			
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335	Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro			
336	35	40	45	
339	Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys			
340	50	55	60	
343	Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys			

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344	65	70	75	80												
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352							100				105				110	
355	Thr	Gln	Cys	Glu	Phe	Ser	Lys	Gln	Glu	Phe	Met	Asp	Gly	Met	Thr	Glu
356							115				120				125	
359	Leu	Gly	Cys	Asp	Ser	Thr	Glu	Lys	Leu	Lys	Ala	Gln	Ile	Pro	Lys	Met
360							130				135				140	
363	Glu	Gln	Glu	Leu	Lys	Glu	Pro	Gly	Arg	Phe	Lys	Asp	Phe	Tyr	Gln	Phe
364							145				150				155	
367	Thr	Phe	Asn	Phe	Ala	Lys	Asn	Pro	Gly	Gln	Lys	Gly	Leu	Asp	Leu	Glu
368							165				170				175	
371	Met	Ala	Ile	Ala	Tyr	Trp	Asn	Leu	Val	Leu	Asn	Gly	Arg	Phe	Arg	Leu
372							180				185				190	
375	Leu	Asp	Leu	Trp	Asn	Lys	Phe	Leu	Leu	Glu	His	His	Lys	Arg	Ser	Ile
376							195				200				205	
379	Pro	Lys	Asp	Thr	Trp	Asn	Leu	Leu	Leu	Asp	Phe	Ser	Thr	Met	Ile	Ala
380							210				215				220	
383	Asp	Asp	Met	Ser	Asn	Tyr	Asp	Glu	Glu	Gly	Ala	Trp	Pro	Val	Leu	Ile
384							225				230				235	
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407	<223>	OTHER INFORMATION:	DNA nucleotide sequence encoding the siRNA construct													
		designed to														
408		target	expression	of	the	SCCRO	gene									
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,622

DATE: 05/26/2006

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05262006\J579622.raw

L:27 M:270 C: Current Application Number differs, Replaced Current Application No

L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date